







Db	1505	AGCTGGGGGGCTGAGAGCAACCCAGAGACCGAGGAGACGAGGAGACGAGGAGGCGGACATTGCGGCAATTAC	1567
Oy	1430	ATGGCCAGGTGACTGTCTCCCGGCAATATCCACCGAATCTGATG	1472
Db	1565	ATTGGCCAGGTGACTGTCTCCCGGCAATATCCACCGAATCTGATG	1607
RESULT 3	AF439325	4536 bp	RNA
LOCUS	AF439325		linear
DEFINITION	Homo sapiens putative class II cytokine receptor CRF2/12 (CRF2/12)		PRI 06-NOV-2002
ACCESSION	AF439325		RNA, complete cds.
VERSION	AF439325.1	GI:24637276	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 4536)		
TITLE	Gallagher, G. and Kotenko, S.		
JOURNAL	CRF2/12 is a novel member of the class-II cytokine receptor family		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 4536)		
TITLE	Gallagher, G. and Kotenko, S.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (23-OCT-2001) Dental Research Centre, NIDDS / Dept. of Biochemistry and Molecular Biology, NIDDS, University of Medicine and Dentistry of New Jersey, 185 South Orange Avenue, Newark, NJ 07103-2714, USA		
REMARK	This is joint equal work from G. Gallagher and S. Kotenko		
FEATURES	Location/Qualifiers		
SOURCE	1..4536		
gene	/organism="Homo sapiens"		
CDs	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/chromosome="1"		
	1..4536		
	/gene="CRF2/12"		
	1..1563		
	/codon_start=1		
	/product="putative class II cytokine receptor CRF2/12"		
	/protein_id="AA063632.1"		
	/db_xref="GI:24637272"		
	/translation="MAGDERWGPILLCLQLAAGRPRLAPPONTYLLSDFSVYLTWVPGANPDVTVFAVYQSPTRRRAREVEBCAGKELLSMCKLQDLVNRKGVRFVSPSSPMWSEYEDLYDFEVEAPAPLVLTOTESIISANATYDLPKMPDLKYEEAFPMKSGAKKTLFPTVPHGQGPVOTLQAPASHHKLSARTYPSVSKSKSKTCCLATRPANNAKPYLPSLITLITLYTAAGVYVKTITLGNWFRPAMPRALDDESGHNPALTPQSPRESVNDLFLCQKELTRGAREPFRARATQCTRMKDLAEDESEDEDEEDGYSFQPTIEPPSPFLGQEHAPGHSBAGVSGSRAPALVPSGSSAWDSIDRSWATTVQSSWDVAGSSGGLYLAEGPQGGQGGHQLSPPEFSKDSGLBELPEDNLSSWATWGLPEPMLVPGPPVSLQTLTFCWSSPSEEEARESEIEDSDAGSGASTORTYEMARDRGTTGHTMA"		
BASE COUNT	1014 a 1256 c 1204 g 1062 t		
ORIGIN			
Query Match	88.94; Score 1309; DB 9; Length 4536;		
Match Local Similarity	91.64; Pred. No. 0; Mismatches 0; Indels 134; Gaps		
Matches 1463; Conservative	0; Mismatches 0; Indels 134; Gaps		
Oy	7	ATGCGCGGGGCCGAGCGCTGGGGGCCCCCTGCTCTGTGCTGCTGTCGACGAGCGGCTCCAGAGG	66
Db	1	ATGCGCGGGGCCGAGCGCTGGGGGCCCCCTGCTCTGTGCTGCTGTCGACGAGCGGCTCCAGAGG	60
Oy	67	AGGCGCGGCTGCGCCCTCCCGAGAGTGTACGCTGCTCCCGAGAACTTCAGGGTAC	126
Db	61	AGGCGCGGCTGCGCCCTCCCGAGAGTGTACGCTGCTCCCGAGAACTTCAGGGTAC	120
Oy	127	CTGACATGTGCTCCAGGGGCTTGCGCAACCCCGAGATGTGACCTATTGTTGGCCTATCAG	186
Db	121	CTGACATGTGCTCCAGGGGCTTGCGCAACCCCGAGATGTGACCTATTGTTGGCCTATCAG	180

QY	187	AGCTCTCCACCCGGTAGACAGGTGGCCGGAAGTGAAGAGTGTGGGGAACAAGAGCTG	246
Db	181	AGCTCTCCACCCGGTAGACAGGTGGCCGGAAGTGAAGAGTGTGGGGAACAAGAGCTG	240
QY	247	CTAATGTTCTATATATATGCTGAGAGAAAGAGACCTGTATCAACAAGTTCAAGGAGCTCTG	306
Db	241	CTAATGTTCTATATATATGCTGAGAGAAAGAGACCTGTATCAACAAGTTCAAGGAGCTCTG	300
QY	307	CGAGACGGTTCCTCCAGCTCCAGTCCCTCTGGTGAAGTCCGATACCTGGAATTACCTT	366
Db	301	CGAGACGGTTCCTCCAGCTCCAGTCCCTCTGGTGAAGTCCGATACCTGGAATTACCTT	360
QY	367	TTTAAATGAGACCGGCCCCCACTGTCTGTGGTCTCAACCGAGAGAGAGATCCGAGAT	426
Db	361	TTTAAATGAGACCGGCCCCCACTGTCTGTGGTCTCAACCGAGAGAGATCCGAGAT	420
QY	427	GCCAATGCACTGATCAAGCTGCCCCCTCGATGCCCCCACTGATCTGAAGTATGAAGTGTG	486
Db	421	GCCAATGCACTGATCAAGCTGCCCCCTCGATGCCCCCACTGATCTGAAGTATGAAGTGTG	480
QY	487	GCATTCTGAGAGAGGGGGCCGGAACAAGACCTATTTCCAGTCACTCCCACTGCGACAG	546
Db	481	GCATTCTGAGAGAGGGGGCCGGAACAAGACCTATTTCCAGTCACTCCCACTGCGACAG	540
QY	547	CCAAATCCAGATCACTCTCCAGCGACGTCGACGAGGAAACAACAATGCTCAATGCGAAGAAC	606
Db	541	CCAAATCCAGATCACTCTCCAGCGACGTCGACGAGGAAACAACAATGCTCAATGCGAAGAAC	600
QY	607	ATCTACACGTTCAAGTGTCCCGAAATACAGCAAGTTCTTAAAGCCCACTGCTTCTTGCTG	666
Db	601	ATCTACACGTTCAAGTGTCCCGAAATACAGCAAGTTCTTAAAGCCCACTGCTTCTTGCTG	660
QY	667	GAGGTGCCA-----	675
Db	661	GAGGTGCCAAGAACCAACTGGGCTTTCTGTGTGCTGCAATGGCTTCTGATATCTGCTGTTA	720
QY	676	-----	675
Db	721	GTAATTGCCGAGGGGGGTGTGATCTGGAAGACCTTCATGGGAAACCTTGCTTCAAGCG	780
QY	676	-----GACCTTTCTGAGACAACAACCTGTGGCAACTTTTCAG	715
Db	781	GCAAGAATGCAAGGCCCCGTGAACCTTTCTGAGACAACAACCTGTGGCAACTTTTCAG	840
QY	716	CCCAAGCAACAGAGTCCGTGATATGATCTGTTTCTGTGCCCAAAAGGAATGACACAGA	775
Db	841	CCCAAGCAACAGAGTCCGTGATATGATCTGTTTCTGTGCCCAAAAGGAATGACACAGA	900
QY	776	GGGGTCAAGGCCGACGCTGTGAGTCAAGGCCCCCAAGCCCAACAAGACAGATGGAAGAG	835
Db	901	GGGGTCAAGGCCGACGCTGTGAGTCAAGGCCCCCAAGCCCAACAAGACAGATGGAAGAG	960
QY	836	GACCTTCAAGAGACGAAGAGAGAGATATGAGAGAGACACAGAAAGATGGCGTCAAGCTTC	895
Db	961	GACCTTCAAGAGACGAAGAGAGAGATATGAGAGAGACACAGAAAGATGGCGTCAAGCTTC	1020
QY	896	CAGGCCCTACATTGAACAACCTTTCTTCTGTGGGCAAGAGCAACAGGCTCCAGGGGCACTG	955
Db	1021	CAGGCCCTACATTGAACAACCTTTCTTCTGTGGGCAAGAGCAACAGGCTCCAGGGGCACTG	1080
QY	956	GAGGCTTTTGTGTGGGTGATCTCAAGGAGGCCCAAGGCTCTCTTGTTCCCAAGCGAAGCT	1015
Db	1081	GAGGCTTTTGTGTGGGTGATCTCAAGGAGGCCCAAGGCTCTCTTGTTCCCAAGCGAAGCT	1137
QY	1016	TGCTCTGCTTGGGATCTTTCAGACAGAAAGCTGGGCAAGCATGTGGAATCTCTCTGGGAC	1075
Db	1138	TGCTCTGCTTGGGATCTTTCAGACAGAAAGCTGGGCAAGCATGTGGAATCTCTCTGGGAC	1197
QY	1076	AGGGCTGGGCTCTTGGGCTAATTTGGCTGAAGAGGGCCAGAGCGCGGGTGGGAT	1135
Db	1198	AGGGCTGGGCTCTTGGGCTAATTTGGCTGAAGAGGGCCAGAGCGCGGGTGGGAT	1257

```

OY 1136 GGGCACCAGAAATCTCTCCACACCTGAATTCCTCAAGAGCTCGGATTCTTGAGAG 1195
DB 1258 GGGCACCAGAAATCTCTCCACACCTGAATTCCTCAAGAGCTCGGATTCTTGAGAG 1317
OY 1196 CTCCAGAGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1255
DB 1318 CTCCAGAGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1377
OY 1256 CTGGTCCCTGGGAGACCCCGAGTTTCTCTTCAAGACCTGACCTTCTCTGGAGAAAGCAGC 1315
DB 1378 CTGGTCCCTGGGAGACCCCGAGTTTCTCTTCAAGACCTGACCTTCTCTGGAGAAAGCAGC 1437
OY 1316 CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1375
DB 1438 CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1497
OY 1376 GGGGCTGAGAGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1435
DB 1498 GGGGCTGAGAGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1557
OY 1436 AGGTGAGCTGTCTCCCGACATCCACCGAATCTTGATG 1472
DB 1558 AGGTGAGCTGTCTCCCGACATCCACCGAATCTTGATG 1594

RESULT 4
AX478514 1563 bp DNA linear PAT 12-AUG-2002
LOCUS AX478514
DEFINITION Sequence 18 from Patent WO0244209.
ACCESSION AX478514
VERSION AX478514.1 GI:22217286
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Presnell,S.R., Xu,W., Novak,J.E., Whitmore,T.B. and Grant,P.J.
            Cytochrome receptor zcytor19
            Patent: WO 024209-A 18 06-JUN-2002;
            Zymodiagnostics, Inc. (US)
FEATURES
            Location/Qualifiers
            1..1563
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
               1..1563
               /note="unnamed protein product"
               /codon_start=1
               /protein_id="CAD43695.1"
               /db_xref="GI:22217287"
               /translation="MAGPERMGPLLLCLQAAPGRPLAPPOINTLLSOLFVYLLTL
               PGLNPQVITYFVAYOSSPTRRRRRVRBECAGTKELCSMMLCKKODLYNKPGRVRT
               VSPSSKSPVSESYLDLTFVBPAPPLVLTOTBEHLSANATYGLPOMPBLDKYEV
               AFWKGAAGNKLTPVTPHGOPIVOTLOPAASHHCISARTTYTSVPKSKPKPTCF
               LLEVPANMAPIVLPILLILLIYLAAGGTYWTKLGNWTFQAKMPALDPSGTHPV
               ATPQSPRESVNDLPFCQKELTRGVPTVRATVQOTWKKDLADEDEEDBT
               EGVAFQYIIEPSPFLQDQEHQKSHBAGVDSGRAPALVPSGSSAMDSDRVAS
               TYDSSMDPASSSGTLAKRPGQSGDGHQBSLPPRPSSKQSGTLEBIPDNLSWAT
               WQTLPEPBNLVPGPVPVSLQTLTFCWESSPEEBEERBSIEDSDAGSMGAESTQTR
               DGRITLGHYMAR"
CDS
            335 a 468 c 471 g 289 c
BASE COUNT
ORIGIN
Query Match 86.8%; Score 1278; DB 6; Length 1563;
Best Local Similarity 91.4%; Pred. No. 0;
Matches 1432; Conservative 0; Mismatch 0; Indels 134; Gaps 2;

```

```

DB 61 AGGCCCGCTGCGCCCTCCCGAGAAATGTAAGCTGCTCTCCAGAACTTCAGGCTGTAC 120
OY 127 CTGACATGAGCTCCAGGAGCTTGGCAACCCAGAGATGTGACCTATTTGTGGCTTACAG 186
DB 121 CTGACATGAGCTCCAGGAGCTTGGCAACCCAGAGATGTGACCTATTTGTGGCTTACAG 180
OY 187 AGCTTCCCAACCTGTAGACGGTGGCCGAAAGTGAAGTGTGCGGAGACCAAGAGCTG 246
DB 181 AGCTTCCCAACCTGTAGACGGTGGCCGAAAGTGAAGTGTGCGGAGACCAAGAGCTG 240
OY 247 CTATGTTCTATGATGTGCTGAAGAAACAGAGACTGTACCAAGTTTCAAGGAGCGGTG 306
DB 241 CTATGTTCTATGATGTGCTGAAGAAACAGAGACTGTACCAAGTTTCAAGGAGCGGTG 300
OY 307 CGGACGGTTTCTCCAGCTCCAGTCCCTCTGGGTGAGTCCGAATACCTGATTTACCTT 366
DB 301 CGGACGGTTTCTCCAGCTCCAGTCCCTCTGGGTGAGTCCGAATACCTGATTTACCTT 360
OY 367 TTGGAAGTGAAGCCGAGCCCAACCTGTCTGTGCTCAACCAAGAGAGATCTTGAGT 426
DB 361 TTGGAAGTGAAGCCGAGCCCAACCTGTCTGTGCTCAACCAAGAGAGATCTTGAGT 420
OY 427 GCCAATGCCAGTACAGAGTCCCTCTGATGCCCTCACTGAAATCTGAAGTGAAGT 486
DB 421 GCCAATGCCAGTACAGAGTCCCTCTGATGCCCTCACTGAAATCTGAAGTGAAGT 480
OY 487 GCATTTCTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 546
DB 481 GCATTTCTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
OY 547 CCAGTCCAGATCACTCTCCAGAGAGTCCCTCTGATGCCCTCACTGAAATCTGAAGTGAAGT 606
DB 541 CCAGTCCAGATCACTCTCCAGAGAGTCCCTCTGATGCCCTCACTGAAATCTGAAGTGAAGT 600
OY 607 ATCTACAGTTCAGTGTCTCCGAAATACAGCAAGTTCTTGAAGCCCACTCTTCTGCT 666
DB 601 ATCTACAGTTCAGTGTCTCCGAAATACAGCAAGTTCTTGAAGCCCACTCTTCTGCT 660
OY 667 GAGGTCCCA----- 675
DB 661 GAGGTCCCAAGGCAAGCCACTGGGCTTCTGTGCTGCAATGCTTCTGAATCTGTGTTA 720
OY 676 ----- 675
DB 721 GTAAATTCGCGAGAGGAGGTGATCTGAAGACCTCATGAGGAAACCCCTGTGTTCAAGCG 780
OY 676 -----GACCTTTCTGACACACACACCCGTGTGCAACCTTTCAAG 715
DB 781 GCAGAGATGCAAGGAGGCTGTGACCTTTCTGACACACACCCGTGTGCAACCTTTCAAG 840
OY 716 CCCACAGACAGAGTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 775
DB 841 CCCACAGACAGAGTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
OY 776 GGGGTCAGGCGCAGCTCTGAGTCAAGGCGCCAGCCACCAACAGACAGATGGAAGAG 835
DB 901 GGGGTCAGGCGCAGCTCTGAGTCAAGGCGCCAGCCACCAACAGACAGATGGAAGAG 960
OY 836 GACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 895
DB 961 GACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
OY 896 CAGCCTTACATTGAACACCTTTCTTCTGAGGAGAGAGACAGGCTCCAGGAGCACTG 955
DB 1021 CAGCCTTACATTGAACACCTTTCTTCTGAGGAGAGAGACAGGCTCCAGGAGCACTG 1080
OY 956 GAGGCT??TGGTGGGAGTGAATCAAGGAGAGCCAGGAGCTCTCTGAGTCCCAAGCAAGG 1015
DB 1081 GAGGCT---TGGTGGGAGTGAATCAAGGAGAGCCAGGAGCTCTCTGAGTCCCAAGCAAGG 1137
OY 1016 TCTCTGCTGGAGATTTTGAACAGAGCTGGGCAAGACTGTGATCTCTCTGAGAC 1075

```











Db 661 GAGGTCCAGAGCAAGTGGGCTTCTGAGTGTGCTGCAATCGCTTCTGTAAGTCTGTA 720  
Qy 665 CACCTGTGGCACTTTTCAAGCCGAGAGACAGATCCGTAATGACTTTTCTCTGT 754  
Db 721 GTAATTCCGAGGGGGTGTGATCTGGAAGACCTTCAATGGAGAACCCCTGTCTCAGCGG 780  
Qy 755 CCCCMAA-----AGGACTGACAGAGGGGTCAAGCGGCGAGCTTCAAGTCAAG 802  
Db 781 GCMAAGATGCGAGGGGCTTGGATCTGACAGAGGGGTCAAGCGGCGAGCTTCAAGTCAAG 840  
Qy 803 GCGCCAGCCGACCAAGAGCAAGATGAGAGAGAGACTTTGACAGAGAGAGAGAGAG 862  
Db 841 GCGCCAGCCGACCAAGAGCAAGATGAGAGAGAGACTTTGACAGAGAGAGAGAGAG 900  
Qy 863 GATGAGAGAGAGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 922  
Db 901 GATGAGAGAGAGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
Qy 923 CTGGGGGAG 982  
Db 961 CTGGGGGAG 1017  
Qy 983 AGGCGGAG 1042  
Db 1018 AGGCGGAG 1077  
Qy 1043 AGCTGGGCGAG 1102  
Db 1078 AGCTGGGCGAG 1137  
Qy 1103 GAG 1162  
Db 1138 GAG 1197  
Qy 1163 GAATTTCTCCAG 1222  
Db 1198 GAATTTCTCCAG 1257  
Qy 1223 GCGCCTGTGGGAG 1282  
Db 1258 GCGCCTGTGGGAG 1317  
Qy 1283 CTTCAG 1342  
Db 1318 CTTCAG 1377  
Qy 1343 TCAGAAATGAG 1402  
Db 1378 TCAGAAATGAG 1437  
Qy 1403 GACAGGGGCGGAG 1441  
Db 1438 GACAGGGGCGGAG 1476

RESULT 8  
AX478499 1473 bp DNA linear PAT 12-AUG-2002  
LOCUS AX478499  
DEFINITION Sequence 3 from Patent WO0244209.  
ACCESSION AX478499  
VERSION AX478499.1 GI:22217275  
KEYWORDS  
ORGANISM synthetic construct  
SOURCE synthetic construct  
REFERENCE 1. artificial sequences.  
AUTHORS Presnell, S.R., Xu, W., Novak, J.B., Whitmore, T.B. and Grant, F.J.  
TITLE Cytokine receptor zcytor19  
JOURNAL Patent: WO 0244209-A 3 06-JUN-2002;  
ZymoGenetics, Inc. (US)  
FEATURES  
Location/Qualifiers  
1..1473  
source 1..1473  
/organism="synthetic construct"

Query Match 58.5%; Score 861.8; DB 6; Length 1473;  
Best Local Similarity 52.5%; Pred. No. 2.2e-209;  
Matches 775; Conservative 320; Mismatches 333; Indels 47; Gaps 3;  
BASE COUNT 203 a 195 c 278 g 164 t 633 others  
ORIGIN  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Degenerate polynucleotide sequence of SEQ ID NO:2"  
7 ATGGCGGGGCGGAG 66  
1 ATGGCGGGGCGGAG 60  
Qy 67 AGGCGGCGGCGGAG 126  
Db 61 AGGCGGCGGCGGAG 120  
Qy 127 CTGACATGAG 186  
Db 121 CTGACATGAG 180  
Qy 187 AGCTCTCCAG 246  
Db 181 AGCTCTCCAG 240  
Qy 247 CTATGTTCTATGAG 306  
Db 241 CTATGTTCTATGAG 300  
Qy 307 CGGAG 366  
Db 301 CGGAG 360  
Qy 367 TTTGAG 426  
Db 361 TTTGAG 420  
Qy 427 GCGAATGCGAG 486  
Db 421 GCGAATGCGAG 480  
Qy 487 GCAATCTGAG 546  
Db 481 GCAATCTGAG 540  
Qy 547 CCAATGCGAG 606  
Db 541 CCAATGCGAG 600  
Qy 607 ATCTACAG 666  
Db 601 ATCTACAG 660  
Qy 667 GAGGTCCAG 721  
Db 661 GAGGTCCAG 720  
Qy 722 -----AGACAG 780  
Db 721 GATGAG 780  
Qy 781 GATGAG 840  
Db 781 GATGAG 840  
Qy 803 GCGCCAGCCGACCAAG 862  
Db 841 GCGCCAGCCGACCAAG 900  
Qy 863 GATGAG 922  
Db 901 GATGAG 960

Qy	923	CTGGGGGCAAGAGCAACGAGGCTCAAGGGACATCCGAGAGCT??TGGGGGGGTGGACTCAAGG	982
Db	961	YTNNGNCAAGARCAATGACGNCNGAGCAATMSNGAGC---NGNGGNGTNGAYMSNGN	1017
Qy	983	AGGCCCAAGGCTCTCTGGTCCCAAGCAAGGCTCCTCTGCTTGGGATTTCTTCAACAGA	1042
Db	1018	MGNCCNMGNGCNCNTTNGTNCNMSNGAGGMSWSNGCNTGGGAYMSWSNGAYMGN	1077
Qy	1043	AGCTGGGCAAGCACTGTGACTCTCTCTGGGCAAGGCTGGGCTCCTCTGAGCTATTTGGCT	1102
Db	1078	WSNTGGGCMNSMNCNTTNGAYMSWSNTGGGATMGNGCNGGMSWSWSNGTATYTTNGCN	1137
Qy	1103	GAGAAAGGGGCAAGGCCAAGGGCCGGGATGGGATGGGCACCAAGATCTCTCCACACT	1162
Db	1138	GABAAAGGNCNGGNCARAGNCNGAGNGGNDATGGNCAYCARGAMSNTTNCNCNCN	1197
Qy	1163	GAATTTCTCCAAAGACATCGGGTTTCTGTGAAGAGCTCCCAAGAAATACATCTCTCTCGG	1222
Db	1198	GAATTTSMNAAAGAYMSNGATTTTNGARARXTTNCNGARAGATAAATTTMSMSNTGG	1257
Qy	1223	GCCACTTGGGGCACTTACCAACCGGAGCCGAATCTGGTCCCTGGGGGACCCCAATTCT	1282
Db	1258	GCNAATGGGGMNCNTTNCNCNGARCNAAATYTTGTTNCNCGNGGNCNCNCNGTMSN	1317
Qy	1283	CTTCCAGACATGACCTTCTGTGTGGGAAAGCAGCCCTGAGAGGAGAGAGAGGAGA	1342
Db	1318	YTNCPACNTYTNACNTTYYTGYGGGARMSWSMNSNCNGAGAGAGAGAGGAGNCNGAR	1377
Qy	1343	TCAGAAATTGGAGACGATCCGGGGCAGCTGGGGGGCTGAGAGCACCCAGAGAACGAG	1402
Db	1378	WSNGARATHGARBAYSMSNATGCTNGGMSNTYGGGNGCNGAARMSNACNCAKMGNAENGAR	1437
Qy	1403	GACGAGGGCCGACATTGGGGCATTAATCATGCGCAG	1437
Db	1438	GAATMGNGMGNACNTTNGCNCATYATATGCGCNGG	1472

RESULT 9					
LOCUS	AX478524	1560 bp	DNA	linear	PAT 12-AUG-2002
DEFINITION	Sequence 28 from Patent WO0244209.				
ACCESSION	AX478524				
VERSION	AX478524.1	GI:22217296			
KEYWORDS					
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	artificial sequences.				
AUTHORS	1				
TITLE	Prenell,S.R., Xu,W., Novak,J.E., Whitmore,T.E. and Grant,F.J.				
JOURNAL	Cyclokin receptor zyclocl19				
	Patent: WO 0244209-A 28 06-JUN-2002;				
	Zymogenetics, Inc. (US)				
FEATURES	Location/Qualifiers				
source	1	1560			
	/organism="synthetic construct"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:32630"				
	/note="Generate Polynucleotide sequence of SEQ ID				
	NO.19"				
BASE COUNT	221 a	209 c	286 g	173 t	671 others
ORIGIN					

	Query Match	Similarity	Score	DB	Length
Qy	Best Local	51.9%	852.6	6	1560
	Matches	810	Conservative	331	Mismatches 287; Indels 134; Gaps 2;
Db	1	ATGGGNGGNCNGMAGMGTGGGNCNTNTNTNTNTGTYTTCACGCGNCNCNGAN	60		
Qy	7	ATGGGGGGGCGCAGAGCGTGGGCGCCCGCTGCTGCTGCTCAGAGCCGCTCAGAGG	66		
Db	67	AGGCGCCGTCTGGGCCCTCCCAAGATGACGTGCTCTCCCAACATTACGGTGTAC	126		

D6	61	MGNCGNNGNTGNCNCNCNCACBAAVGTNA	CNTYTNMNSCARAAVYTNMNGNTAY	120	
OY	127	CTGACATGGCTCCCAAGGGCTTGGAACCC	CCAGAGATGACCTATTTTGGGCTATCAG	186	
D6	121	YTNACNTGGTTCNCNGNNTTGGNAATCC	NCARAGVGTNACNTATYTTGTGNCNTAYCAR	180	
OY	187	AGCTCTCCCAACCCGTAGACGGTGGCGAA	AGTGGAAAGTGGCGGACCAAGAGCTG	246	
D6	181	MSNSNCNCA	CNNNGNNGNTGCGNGAGTNGAGARTYGC	240	
OY	247	CTAAGTCTATGATGTGCTGTAGAGAAAC	AGACCTGTCAACAAGTTCAGAGGACGGCTG	306	
D6	241	YTNMGYSNATGATGTGTATTAADBAAC	AGAGATYTNATAVAAARTTYAARGMNGNTN	300	
OY	307	CGAGAGGTTTCTCCCAAGCTCCCAAGTCCC	CCGTGGTGGAGTCCGAAATACCTGATACCTT	366	
D6	301	MGNACNGTMSNCCNMSNSNABASNC	CNTGGGTGAGMSGARTAYTNAGATYATYN	360	
OY	367	TTTAAATGAGAGCGGAGCCCAACTGTGT	CTGTGCTCACCACAGAGAGAGATCCTGACT	426	
D6	361	TTYAGRTGNARCNCGNCNC	CNGTNTYTNGTNTYTNACACARACNGARARATHYMSN	420	
OY	427	GCACATGCACGTACAGATGGCCCCCTGT	ATGCCCACTGAGATCTGAAGTATGAGTG	486	
D6	421	CGMAAYGQNDTAYACARTMCCNC	CNTGTATGCGNCCMYTNAGAYTNABARTYAGRTN	480	
OY	487	GCAATCTCGAAGAAGGGGCGGAAACAA	ACCTATTTCACAGTCACTCCCACTGGCCAG	546	
D6	481	GCATTTGGAARARAGNCNGNNAATAA	CNTTNTTTCNGTACNCCNCAVGCNCAR	540	
OY	547	CCAGTCAGATCACTCTCCAGACAGCTGC	ACAGGAAACAACAATCCTCACTGTCAGAGAAC	606	
D6	541	CCNGTNCBARATTHACNTYTNAC	CCNGCNGMBSNGARCAVATGTGTYNMSNGCMGNACN	600	
OY	607	ACTTACACAGTTGAGTGTCCGAAATTA	CAGCAATGTTCTTAAAGCCCACTCTCTTGCTG	666	
D6	601	ATHTAYACNTTYSNTTNCNABATTA	YMSBAATTTYSNABRCNACNTGTYYTNTYN	660	
OY	667	GAGTCCCAAG-----		676	
D6	661	GARGTNCNGARCNAAVYGGCNTTYT	YTNGTNTNCCNMSYNTYTNATHYTNNTYN	720	
OY	677			676	
D6	721	GTNATHGCGNCNGANGNTNATHGAA	AAACNTNATGGGAAVCCNTGTTCYARBGN	780	
OY	677	-----		676	
D6	781	GCNABARTGCCNMGNCNTNGATYTT	YSNGNCAACNCAICGNTGNCNACNTTYCAR	840	
OY	716	CCAGACGACACAGAGTCCGTATATG	ACTCTTCTCTGTCCCAAAAGAACTGACACA	775	
D6	841	CCNMSNNGNCNABRNSNTNNAAYGA	YVYTTTYTNTGTCNCAARBARGARVYTNACMGN	900	
OY	776	GGGGTCAGGCGCAGGCTCGATCAGAGG	CCCCCAGCCACCAACAGACATAATGGAAGA	835	
D6	901	CGNGTNGNCCNACNCGNNGTMMGNC	CCNAGCAACARACAMGNTGGAABAR	960	
OY	836	GACCTTGACAGAGCAAGAGAGAGAT	TGAGAGAGACACAGAAATGCGCTCAGCTTC	895	
D6	961	GATYTNCGNARARAYARBARCARAG	ATGAAGAATACNGARATGAGNTMSNTTY	1020	
OY	896	CAGCCTTACATTGAACACCTTCTT	TCTCTGGGAGAGACAGACCAAGGCTTCA	955	
D6	1021	CARCCNTAYATHGARCMNC	CMWSYTYTNTGNCAGARCAVACARGCCNCGNCAYMSN	1080	
OY	956	GAGGCTTTTGGTGGGTGATCTCAG	AGGAGGCCCAAGGCTCTCTGCTCCCAAGCAGGC	1015	
D6	1081	GARGC-----	NGNGBNTNDATYMSNGMNGCCMAGNCCN	CMYTNGTNCCMBSNGARGN	1137
OY	1016	TCTCTGTGTTGGGATTTCTT	CAGACAGAACTGGGCCAGACCTGTGAC	CTCTCTTGGGAC	1075
D6	1138	MSNNSNGCNTGGATYMSNMSNDATY	MGMSNTTGGCCNMSACGNTGAGATYMSMSNTTGGAGV	1197	



QY 1334 GCGAGGAATCAGAAATTGAGACACGATGCGGCGAGCTGGGGGCTGAGAGACACCAG 1393  
 DB 21836 GCGAGGAATCAGAAATTGAGACACGATGCGGCGAGCTGGGGGCTGAGAGACACCAG 21777  
 QY 1394 AGGACCGAGGACAGGGGCGGACATTGGGGCAATTATGCGGAGGTAGCGTCCCCCA 1453  
 DB 21776 AGGACCGAGGACAGGGGCGGACATTGGGGCAATTATGCGGAGGTAGCGTCCCCCA 21717  
 QY 1454 CATCCACCGAATCTGATG 1472  
 DB 21716 CATCCACCGAATCTGATG 21698

RESULT 11  
AX478518

LOCUS AX478518 1422 bp DNA linear PAT 12-AUG-2002  
 DEFINITION Sequence 22 from Patent WO0244209.  
 ACCESSION AX478518  
 VERSION AX478518.1 GI:22217290

## KEYWORDS

SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1  
 AUTHORS Presnell,S.R., Xu,W., Novak,J.E., Whitmore,T.E. and Grant,F.J.  
 TITLE Cytokine receptor zcytor19  
 JOURNAL Patent: WO 0244209-A, 22 06-JUN-2002;  
 Zymogenetics, Inc. (US)

## FEATURES

source 1..1422  
 location/Qualifiers  
 1..1422  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="Zcytor19-Fc4 fusion protein"  
 1..1422  
 /note="unnamed protein product"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="CAD43697.1"  
 /db\_xref="GI:22217291"

## CDS

1..1422  
 /note="unnamed protein product"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="CAD43697.1"  
 /db\_xref="GI:22217291"  
 /translation="MDAMKRGKLCVLLCGAVFSLSGEITHAELRRRPRRLAPQ  
 NTLISQNSFVLTLMPLGAGNPDQVTVFAVQSSPTRRREVEECAGTKELCSMC  
 LKQDLNKRKGRVTVSPSSKSPWSESYDYLFEVPRAPVLYLTQREILSNAT  
 YOLPRCPPLDLKTVAPFKESGAKNTLPPTTSGQVQITLQPAASEHCSARTIT  
 TSVPTKSKSKFTCLFLEPEANRMSDKHTCPCPAPASGASVFLPFRKDT  
 LMSRTREVTCVVDVSHEDPEVKNWYVDGVEVNAKTKREQVNSYRVSVLTV  
 LHMPLNGKSKKCVSNKALPSIKETISKAGQPRSPQVYTLPPSRDELTKQVSLT  
 CLVNGFVPSDIAVEMESNQPENNYKTPPVLDSDGSFPLYSKLTVDKRWQGVNFS  
 CSVNGEALHHNHYTKSLSPGK"

BASE COUNT 331 a 451 c 377 g 263 t  
 ORIGIN

Query Match 41.6%; Score 612.8; DB 6; Length 1422;  
 Best Local Similarity 98.9%; Pred. No. 1.1e-145;  
 Matches 617; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 67 AGGCCCCCTGCGCCCTCCCGAGAAATGAGCGTCTCTCCCGAAGATTCAAGCTGTATC 126  
 DB 109 AGGCCCCCTGCGCCCTCCCGAGAAATGAGCGTCTCTCCCGAAGATTCAAGCTGTATC 168  
 QY 127 CTGACATGCTCCGAGGCTTGGCAACCCCGAGATGACCTATTTTGGGCTATCAG 186  
 DB 169 CTGACATGCTCCGAGGCTTGGCAACCCCGAGATGACCTATTTTGGGCTATCAG 228  
 QY 187 AGCTCTCCACCCCTAGACGCTGCGCGAAGTGAAGAGTGTGCGGAAACCAAGAGCTG 246  
 DB 223 AGCTCTCCACCCCTAGACGCTGCGCGAAGTGAAGAGTGTGCGGAAACCAAGAGCTG 288  
 QY 247 CTATGTTCTATGATGTGCTGAGAAACAGACCTGTCAACAGTTTCAAGGGACGGTG 306  
 DB 289 CTATGTTCTATGATGTGCTGAGAAACAGACCTGTCAACAGTTTCAAGGGACGGTG 348

QY 307 CGAGCGTTTCTCCAGCTCCAAAGTCCCCCTGGGTGAGTCCGAAATACCTGATTAACCTT 366  
 DB 349 CGAGCGTTTCTCCAGCTCCAAAGTCCCCCTGGGTGAGTCCGAAATACCTGATTAACCTT 408  
 QY 367 TTTGAAGTGAAGCGGCGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426  
 DB 409 TTTGAAGTGAAGCGGCGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468  
 QY 427 GCGAATGCCAGTACAGTGTGCCCCCTCGATGCCCCCACTGAGTCTGAAGTATGAGGTG 486  
 DB 469 GCGAATGCCAGTACAGTGTGCCCCCTCGATGCCCCCACTGAGTCTGAAGTATGAGGTG 528  
 QY 487 GCATTTGGAAGAGGAGGCGGCGGAAACCAAGCCCTATTTTCAGTCACTGCCATGAGGCGAG 546  
 DB 529 GCATTTGGAAGAGGAGGCGGCGGAAACCAAGCCCTATTTTCAGTCACTGCCATGAGGCGAG 588  
 QY 547 CCACTCCAGATCACTCTCCAGCGAGCTGCGCAGGACACCACTGCTCACTGCTCCAGAAC 606  
 DB 589 CCACTCCAGATCACTCTCCAGCGAGCTGCGCAGGACACCACTGCTCACTGCTCCAGAAC 648  
 QY 607 ATCTACAGCTTCAGTGTGCGGAAATACAGCAAGTTCTTAAGCCGACCTGCTTCTGCTG 666  
 DB 649 ATCTACAGCTTCAGTGTGCGGAAATACAGCAAGTTCTTAAGCCGACCTGCTTCTGCTG 708  
 QY 667 GAGTCCCGAGAGACTTTTCTGACCA 690  
 DB 709 GAGTCCCGAGAGACTTTTCTGACCA 732

RESULT 12  
AX478528

LOCUS AX478528 1922 bp DNA linear PAT 12-AUG-2002  
 DEFINITION Sequence 32 from Patent WO0244209.  
 ACCESSION AX478528  
 VERSION AX478528.1 GI:22217300

## KEYWORDS

SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1  
 AUTHORS Presnell,S.R., Xu,W., Novak,J.E., Whitmore,T.E. and Grant,F.J.  
 TITLE Cytokine receptor zcytor19  
 JOURNAL Patent: WO 0244209-A, 22 06-JUN-2002;  
 Zymogenetics, Inc. (US)

## FEATURES

source 1..1922  
 location/Qualifiers  
 1..1922  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="MBP-human zcytor19 fusion protein polynucleotide  
 sequence"  
 123..1922  
 /note="unnamed protein product"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="CAD43698.1"  
 /db\_xref="GI:22217301"

## CDS

123..1922  
 /note="unnamed protein product"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="CAD43698.1"  
 /db\_xref="GI:22217301"  
 /translation="MTKEBGLVITWINGDGYNGLAEVKKEFKDGTGKTVFHPDL  
 EEKFPQVATGDPDPIIFMAHDFGGVAGSGLABITDPAKAPOKLVPFTMDVAVRG  
 KLAIVAYEALSLIYKDKLIPNDPKTWBITALDKELKAGSKALNPILOEYFVMP  
 LIAADGVAFTKBNKQDIDYDGVNDAAGAGLTPLVDLIRKHMNDVDTYSIABAP  
 NKERTAMTINGNMANSDITDSKNTGCTTLPFKQPSKPPVGLSLAGTINASPNTEL  
 AKSEFLNLTLDGELAVNKKDKPLGAVALSIFEEADKDPRLATMENOAGEIMRTY  
 POKSAFWAVRVAVTNASSGQTVDEBALDQATNDSHHHHHANSVPLVPRSRPRL  
 APPQNTVLLSQNFVYLTWLPGLGNPDQVTVFAVQSSPTRRREVEECAGTKELC  
 SMCCLKQDLYNKRKGRVTVSPSSKSPWSESYDYLFEVPRAPVLYLTQREILS  
 ANATYQLPKCPPLDLKTVAPFKESGAKNTLPPTTSGQVQITLQPAASEHCSARTIT  
 RTVTPSVTKSKSKFTCLFLEPEANRMSDKHTCPCPAPASGASVFLPFRKDT

BASE COUNT 503 a 517 c 503 g 399 t  
 ORIGIN

Query Match 41.5%; Score 611.6; DB 6; Length 1922;  
 Best Local Similarity 97.0%; Pred. No. 2.2e-145;



Mon Sep 22 11:34:33 2003

us-10-026-106a-9.rge

Page 14

D	598	GTCTTACCTTAATTGACATTAAAGTCAAGCCAGGTTCTGAGCCAGCTGACCTTCTTA	657
Q	667	GAGGTCCCA-----	675
D	658	GAGGCTCCAGGGGACAAAGAGCTGCTCGGCAATGCCCTCACTCTGCTCTAATGATA	717
Q	676	-----	675
D	718	GCAGCCGTGGCAGCAGGTGTGCATGGAAGATAATGAAGAAACCCCTGGTTCAAGGG	777
Q	676	-----GACCTTTCTGGAACAACAACCTGTGGCAACTTCAAG	715
D	778	GTGAAGAGCCGCCGGGCACTGGACTTTTCTGAATACAGATACCCAGTGGCAACTTTCAG	837
Q	716	CCCAACAACCAAGTCCGTGAATGACTTTGTTCTGTCTCCCAAGAAAGAACTGACCA	775
D	838	CCCACTGACCTGAGTTCTCTATGACTTGATCTTTGTCTCCCAAGAAAGAACTGACCA	897
Q	776	GGGGTCAGGCCGACGCTCGAGTCAGGGGCCCAAGCCCAACAACAAGATGGAGAAG	835
D	898	AAGAAACAGGCCAGCCCTCAGGTCAGAAACCAACACACGTACAGGACAGACAAAG	957
Q	836	GACCTTGAAGAGACAAAGAGAGAGAGATAGAGAGACACAGAAATGGCTGTCACTTC	895
D	958	GACACTTCTAGAGATGAAGACAGAGACACAACTTACAA--TGACAGAGGTGACAGGCTC	1014
Q	896	CAGCCCTTACATTGAACCACTTCTTTCTGGGGCAAGAGACCAAGGCTCCAGGGCACTCG	955
D	1015	CAGCCCTTACCTGGAACCGGCCCTCTTCAATCAGCAGAGAGCCCGGGTTATGAAACCTCG	1074
Q	956	GAGGCTTTTG---GTGGGGTGACACTCAGAGAGGCCAGGGCTCTCTGTGTCCCAAGGA	1012
D	1075	GAGACAGACAGACTGTGGGGTGAATTCAGGGGGGCTTGAACATCCCAAGTGGAGAGAC	1133
Q	1013	GCTCTCTCTGTTTGGGATTTCTTCAACAAGAGCTGGGCCCACTGTGACTCTCTCT--	1076
D	1135	GGCTCTCTCTGTGATGGAACTCTTCAACAAGAGCTGGTCCAGCAACAGGGGACTCTCAAT	1194
Q	1071	-GGGACAGGGCTGGGTCTCTGGCTAATTTGGCTGAGAAAGGGGACAGGGCCAGGGG	1122
D	1195	AAGATGAAAGTTGGGTCTTCAAGCTGTTTGAACCAAGAGACCCGACACAGGCCCTGT	125
Q	1130	GGGGAATGGGACCAAGAAATCTCTCCACACACTGTAATTTCTCAAGAGCTCGGGTTCTG	1188
D	1255	GGGGAATGGGCTCCAGAGGCTCTCCCAAGCTGTGAATTTCTGAGAACTTGGGGACCGTG	1314
Q	1190	GAAAGCTCCCAAGAAATTAACCTCTCTCTGGGGCCACTGGGGGCACTTACACAGGAG	1248
D	1315	GAAAGCCTCTGAAGAGATGAGCTCTCGGGGTGAGGATTTCTGATTCTTAATCTCAAG	1374
Q	1250	CCGAATCTGGTCCCTGGGGAAACCCCAATTTCTTCAACACTGACTTGTGTGGGA	1308
D	1375	AAGATCTGGTCTCTGTGAGCCCCCAAGTTCTTTCACAACCTACTTCTCTGGGTC	1434
Q	1310	AGCAGCCT-----GAGGAGGAA	1327
D	1435	AACATCTCTGAGGGGAGAGAGGAAACAGAGGACGAGAGGAAGAGAGAGAGAGAGAG	1494
Q	1328	GAGAGGCGAAGGATTCAGAAATTGAGGACAGGAGTGGGGGCACTGGGGGGCTGAGAC	1387
D	1495	GAGGAAGATGGGATTCAGAACTTAAGGGCAGCAATGCCGCTGTGTGGGCACTTCAAC	1554
Q	1388	ACCCAGAGACCGAGGACAGGGGGCCGACATTTGGGGCATTAATGAGCCAGGTGA	1441
D	1555	GTGACAGAGACGAGAGTCAAGGGGCCGAGATGTGGGAGATTAATTGTGTACAGTGA	1608

RESULT 14	LOCUS	AX478516	674 bp	DNA	linear	PAT 13-AUG-2002
DEFINITION	Sequence 20 from Patent	AX478516	MOO244209.			
ACCESSION		AX478516.1	GI:2221788			
VERSION						

```

KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Prenenell,S.R., Xu,W., Novak,J.E., Whitmore,T.E. and Grant,P.T.
TITLE
Cytokine receptor zcytor13
JOURNAL
Patent: WO 0244209-A 20.06-JUN-2002;
ZymoGenetics, Inc. (US)
FEATURES
source
1..674
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
CDS
1..636
/note="unnamed protein product"
/codon_start=1
/protein_id="Cpda3696.1"
/db_xref="gi:2217289"
/rna_annotation="MAGPERMGPLLCLLOAAPPRLAPPPVTLTSGNSFVITLW
PGANQADITFVAQSFTRRRKREVEACGTBELLSMCCLKDDLYNRKGVRT
VSSRSASVASESTIDITFEVEPAPVIVLTQTEILISANATYQPCPPMPLDTKTB
AFMRGAGKVGSSPPAPRRGLPLPLPLPLRFPSPAPAPAPLLOEVFVHS"
BASE COUNT
128 a 223 c 182 g 141 t
ORIGIN

```

[illegible]

RESULT 15	AY129153	674 bp	mRNA	linear	FBI 26-NOV-2002
LOCUS	AY129153				
DEFINITION	Homo sapiens interleukin 28 receptor A splice variant 3 (IL28RA) mRNA, complete cds; alternatively spliced.				

Accession	Version	Keywords	Source	Organism
AY129153	AY129153.1	GI:25527135		Homo sapiens (human)
Reference Authors				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Title Journal				Sheppard, P.O., Presnell, S.R., Fox, B.A., Gilbert, T., Haldeman, B.A. and Grant, P.J. IL28RA splice variant 3 Unpublished 2 (bases 1 to 674)
Authors				Sheppard, P.O., Presnell, S.R., Fox, B.A., Gilbert, T., Haldeman, B.A. and Grant, P.J.
Title				Direct Submission Submitted (05-JUN-2002) Bioinformatics, ZymoGenetics, Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA Location/Qualifiers
Features				1..674 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"
gene				1..674 /gene="IL28RA" /note="synonym: zcytor19"
CDS				1..636 /gene="IL28RA" /note="alternatively spliced" /codon_start=1 /product="interleukin 28 receptor A splice variant 3" /protein_id="AA28226.1" /db_xref="GI:25527136" /translation="MAGPERWGPILLCLLQAPGRPLRAPPNVTLISONSIVYLITWLPGLSNPDDVTYFVAQSSPTMRKREVEACGTKEILCSMMICKODLYNKKRVRTVSFKSSPWVESYLDIYLFEEVPAPLPVALTYTBSILSNANATQLPCHMPDLIDIKEVAFMEGAKGNKVSSPPARPLPHPLRPSPSPQAPAPLLQBVFPVHS"
BASIS COUNT	128 a	223 c	182 g	141 t
ORIGIN				
Query Match		34.6%	Score 510;	DB 9; Length 674;
Best Local Similarity		100.0%;	Pred. No. 2.3e-119;	
Matches 510;	Conservative	0;	Mismatches	0; Indels
			Gaps	0;
Dy	7 ATGGCGGGGCCGAGCGCTGGGGCCCCCTGCTCTGTGCTCTGCCTGCAGCGCCGTCACAGG	66		
Dd	1 ATGGCGGGGCCGAGCGCTGGGGCCCCCTGCTCTGTGCTCTGCCTGCAGCGCCGTCACAGG	60		
Oy	67 AGGCCCGGTCTGGGCCCCCTGCCAGAATGTACCTGCTCTCCAGAACTCAGCGTGAC	126		
Dd	61 AGGCCCGGTCTGGGCCCCCTGCCAGAATGTACCTGCTCTCCAGAACTCAGCGTGAC	120		
Oy	127 CTGAATGGCTCTCAGAGGCTTGGCAACCCCACAGATGTACCTATTTTGTGGCTATCAG	186		
Dd	121 CTGAATGGCTCTCAGAGGCTTGGCAACCCCACAGATGTACCTATTTTGTGGCTATCAG	180		
Oy	187 AGCTCTCCACCCGTATGACGGTGGGGGAGTGTGAAGTAGTGGGGGAGAACAGAGAGCTG	246		
Dd	181 AGCTCTCCACCCGTATGACGGTGGGGGAGTGTGAAGTAGTGGGGGAGAACAGAGAGCTG	240		
Oy	247 CTAATGTTCTAATGATGCTGCTGAGAAAGAGAGACTGTACACAAGTTCAAGGACCGCTG	306		
Dd	241 CTAATGTTCTAATGATGCTGCTGAGAAAGAGAGACTGTACACAAGTTCAAGGACCGCTG	300		
Oy	307 CGGACGGTTTTCTCCAGCTCCAAGTCCCCCGGGGGTGAATCGGAATACTGTGATTAACCT	366		
Dd	301 CGGACGGTTTTCTCCAGCTCCAAGTCCCCCGGGGGTGAATCGGAATACTGTGATTAACCT	360		
Oy	367 TTGTAAGTGAAGCGGCGCCCAACTGTCTGTGGTGTCACTCCAGACGAGAGATCTTGAAT	426		
Dd	361 TTGTAAGTGAAGCGGCGCCCAACTGTCTGTGGTGTCACTCCAGACGAGAGATCTTGAAT	420		
Oy	427 GCCAATGCCATGACGATGCCCCCGCTGATCCCCCACTGATCTGAAGTATGAGGTG	486		

D<sub>b</sub> 421 GCCAATGCGACGTAACGAGTCCCTCCCTCGATGCCCCCACTGGAATCGAATGAGGTG 480

Q<sub>7</sub> 487 GCATTCTGGAGAGGGGGCCGGAAACAG 516

D<sub>b</sub> 481 GCATTCTGGAGAGGGGGCCGGAAACAG 510

Search completed: September 17, 2003, 20:57:17  
Job time : 3634.68 secs